

ATGGAATTTAGCGGCCGCGAATTCGCCCTTAAG M S Q P K K R K L E S SEQ ID NO:2
ATG TCG CAG CCC AAG AAA AGA AAG CTT GAG TCG SEQ ID NO:1
↑SEQ ID NO:3→

G G G G E G G E G T E E E D G A E R E A 31
GGG GGC GGC GGC GAA GGA GGG GAG GGA ACT GAA GAG GAA GAT GGC GCG GAG CGG GAG GCG 93

A L E R P R R T K R E R D Q L Y Y E C Y 51
GCC CTG GAG CGA CCC CGG AGG ACT AAG CGG GAA CGG GAC CAG CTG TAC TAC GAG TGC TAC 153

S D V S V H E E M I A D R V R T D A Y R 71
TCG GAC GTT TCG GTC CAC GAG GAG ATG ATC GCG GAC CGC GTC CGC ACC GAT GCC TAC CGC 213

L G I L R N W A A L R G K T V L D V G A 91
CTG GGT ATC CTT CGG AAC TGG GCA GCA CTG CGA GGC AAG ACG GTA CTG GAC GTG GGC GCG 273

G T G I L S I F C A Q A G A R R V Y A V 111
GGC ACC GGC ATT CTG AGC ATC TTC TGT GCC CAG GCC GGG GCC CGG CGC GTG TAC GCG GTA 333

E A S A I W Q Q A R E V V R F N G L E D 131
GAG GCC AGC GCC ATC TGG CAA CAG GCC CGG GAG GTG GTG CGG TTC AAC GGG CTG GAG GAC 393

R V H V L P G P V E T V E L P E Q V D A 151
CGG GTG CAC GTC CTG CCG GGA CCA GTG GAG ACT GTA GAG TTG CCG GAA CAG GTG GAT GCC 453

I V S E W M G Y G L L H E S M L S S V L 171
ATC GTG AGC GAG TGG ATG GGC TAC GGA CTC CTG CAC GAG TCC ATG CTG AGC TCC GTC CTC 513

H A R T K W L K E G G L L L P A S A E L 191
CAC GCG CGA ACC AAG TGG CTG AAG GAG GGC GGT CTT CTC CTG CCG GCC TCC GCC GAG CTC 573

F I A P I S D Q M L E W R L G F W S Q V 211
TTC ATA GCC CCC ATC AGC GAC CAG ATG CTG GAA TGG CGC CTG GGC TTC TGG AGC CAG GTG 633

K Q H Y G V D M S C L E G F A T R C L M 231
AAG CAG CAC TAT GGT GTG GAC ATG AGC TGC CTG GAG GGC TTC GCC ACG CGC TGT CTC ATG 693

G H S E I V V Q G L S G E D V L A R P Q 251
GGC CAC TCG GAG ATC GTT GTG CAG GGA TTG TCC GGC GAG GAC GTG CTG GCC CGG CCG CAG 753

R F A Q L E L S R A G L E Q E L E A G V 271
CGC TTT GCT CAG CTA GAG CTC TCC CGC GCC GGC TTG GAG CAG GAG CTG GAG GCC GGA GTG 813

G G R F R C S C Y G S A P M H G F A I W 291
GGC GGG CGC TTC CGC TGC AGC TGC TAT GGC TCG GCG CCC ATG CAT GGC TTT GCC ATC TGG 873

F Q V T F P G G E S E K P L V L S T S P 311
TTC CAG GTG ACC TTC CCT GGA GGG GAG TCG GAG AAA CCC CTG GTG CTG TCC ACC TCG CCT 933

F H P A T H W K Q A L L Y L N E P V Q V 331
TTT CAC CCG GCC ACT CAC TGG AAA CAG GCG CTC CTC TAC CTG AAC GAG CCG GTG CAA GTG 993

E Q D T D V S G E I T L L P S R D N P R 351
GAG CAA GAC ACG GAC GTT TCA GGA GAG ATC ACG CTG CTG CCC TCC CGG GAC AAC CCC CGT 1053

R L R V L L R Y K V G D Q E E K T K D F 371
CGC CTG CGC GTG CTG CTG CGC TAC AAA GTG GGA GAC CAG GAG GAG AAG ACC AAA GAC TTT 1113

A M E D * 376
GCC ATG GAG GAC TGA 1128
←SEQ ID NO:3↑

CGGTTGCCCAAGGGGCAATTCGTTTAAACCTGCAGGACTAG

FIG 1

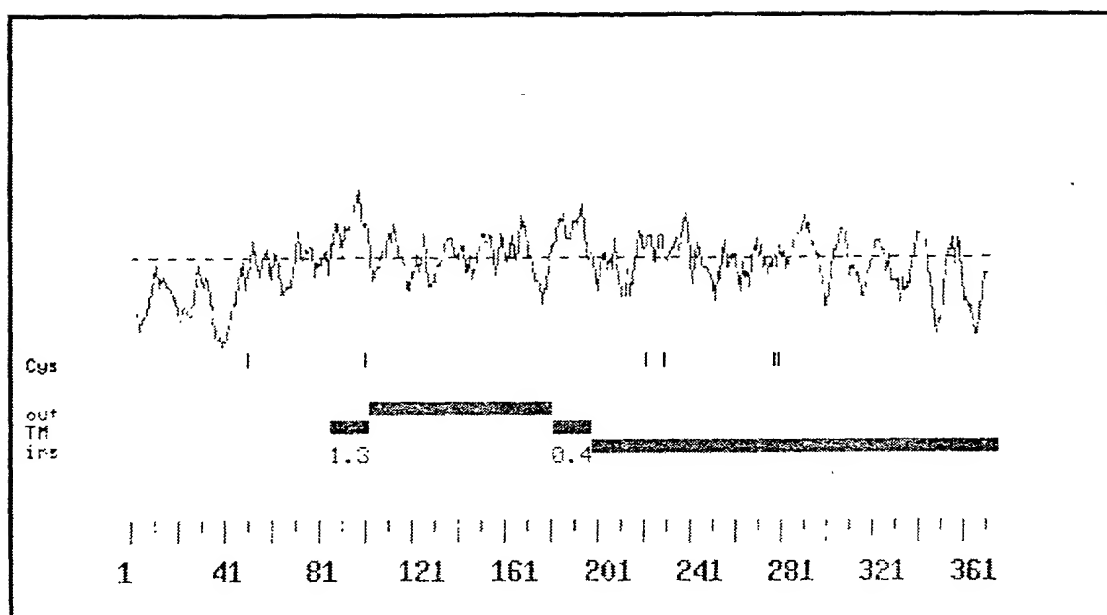


FIG. 2

*->iptsydiiGDivilnipdElrpyrkVigEailkktkkNEMAVvKtVl SEQ ID NO:4
+ +++++ + Ea+l++ ++
27419 19 -----EGTEEDGAEREAALERPRR----- 38
rkkggeedFEGLLGEGYGitGeyRtrrlellLAGekdSGEtvtihkEnGc.r
+ +r++ L+ e +S v +h E + +r
27419 39 ---T-----KRERDQLYYECYS--DVSVEEEMIAdr 64
fkldVsvKVYfSprLegERERlak..lvkeGEvVvDmFAGiGPFsIpiAkh
+ D+ rL + ++ + G +V+D+ AG G sI +A
27419 65 VRTDA-----YRLG-----ILRnwAALRGKTVLDVGAGTGILSIFCAQ- 102
sKakrVyAvdlNPeavkY..LkeNikLNKvedqpKIQTvVNkIipIlgDv
+ a+rVyAv+ ++ +++++e ++ N +ed ++ + g v
27419 103 AGARRVYAVE---ASAIWqqAREVVRFNGLD-----RVHVLPGPV 140
revipekeagvhsIvklvvaDRvi...Mplplarvgqisahefldkalrk
++v++ + + D +++++ M++ l + + + l+ +
27419 141 ETVEL--PE-----QVDAIVsewMGYGL--LHESMLSSVLHARTKW 177
vkdggilvsviHYeflpekaipflpverikraaekeGvkveilkkkrkvk
+k+gg lp++a e ++ a++ + +++
27419 178 LKEGG-----LLLPAASA-----ELFI--APIS----DQMLEWRLG 206
nYaPgvyhvvlDarvn<-*
+ + h+++D +
27419 207 FWSQVKQHYGVDMSCl 222

FIG. 3

Query: 186 PASAELFIAPISD-QMLEWRLGFWSQVKQHYGVDMSCLEGFATRCLMGHSEIVVQGLSGE 244
P L + I D Q + ++ FW V YG +MSC++ A + + +
Sbjct: 1 PDKCTLHLTAIEDTQYKDEKINFWDV---YGFBMSCMKDAAIKEPIVDPKYN-HVVDPN 56 SEQ ID NO:5
Query: 245 DVLARPQRFAQLELSRAGLEQELEAGVGGRFRCSCYGSAPMHGFaiwFQVTF-----PG 298
++ P + ++ + +LE F+ + + +H F WF V F P
Sbjct: 57 QIITDPCTIKEFDMTVKIS-DLETFTSP-FKLTvKRNGMLHAFTAWFDVYFTSKRCHPI 114
Query: 299 GES-EKPLVLSTSPFHPATHWKQALLYLNEPVQVEQDtdVSGEITLLPSRDNPRLRVLL 357
E+ +KP+ ST P P THWKQ + Y+ +P+ V+ + G IT+ ++ N R L + L
Sbjct: 115 PEaIDKPVGFSTGPQSPYTHWKQTIIFYMEDPLPVKTGDTIEGSITISKNNKNNRDLDTL 174
Query: 358 RYKVGdQEEKT 368
+ V +++ T
Sbjct: 175 SWNVNQRQDPT 185

FIG. 4

FIG. 3

Query: 57 HEEMIADRVRTDAYRLGILRNWAALRGKTVLDVGAGTGILSIFCAQAGARRVYAVEAS-A 115
H MI D R +A+ L + R V D+G+GTGILS A+ V A+E +
Sbjct: 142 HIRMINDVKRNEAFAKA-LNDTIKSRTITVVDIGSGTGILSAIAARK-TNLVTALEENMC 199 SEQ ID NO:6

Query: 116 IWQQAREVVRFNGLIEDRVHVLPGPVETVELPEQVDAIVSEWMGYGLLHESMLSSVLHART 175
+ ++EV++ NG+E RV+V E E+ D +VSE + + E ++ + L A
Sbjct: 200 LTMISKEVLKRNGVESRVNVHAKNSTYFETCEKADIVVSETLDCCVFGEKIVETFLDAHV 259

Query: 176 KWLKEGGLLLP 186
++ + + +P
Sbjct: 260 RFSHDRTIFIP 270

FIG. 5

Query: 40 KRERDQLYYECYSDVSVHEEMIADRVRTDAYRLGILRN 77
K + D Y++ Y+ +HEEM+ D VRT++YR I N
Sbjct: 10 KTDDEYYFYFDSYAHYGIHEEMLKDSVRTESYRDFIYHN 47 SEQ ID NO:7

FIG. 6

Query: 43 RDQLYYECYSDVSVHEEMIADRVRTDAYRLGILRNWAAL 81
+D+ Y+ Y + +H EM+AD+ RT Y IL+N +L
Sbjct: 14 QDEEYFGSYGTLKLHLEMLADQPRTTYHVSILQNKESL 52 SEQ ID NO:8

FIG. 7

Query: 75 LRNWAALRGKTVLDVGAGTGILSTFCAQAGARRVYAVEASAIWQQAR-EVVRFNGLIEDRV 133
LR AA+R + LDV G G ++ +S+ W + +V + +G++ +V
Sbjct: 190 LRRQAAIRTDLS-LDV-QGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKV 247 SEQ ID NO:9

Query: 134 HVLPGPVETVELPEQVDAIVSEWMGYGLLHESMLSSVLHARTKWLKEGGLLLPASAELEFI 193
+ + LP + W E+ S L W+ G LLP+S E +
Sbjct: 248 S-----KHIRLPAPCPGLEPSWAKDP--PETRSSLELDTELSWIS--GDLLPSSQEEPL 297

Query: 194 AP-----ISDQMLEWRLGFWWSQVKQHYGVDMSCLE-GFATRCLMGHSEIVVQGLSGE 244
P + Q R GFW ++ + + +SCL+ G R S + Q L G
Sbjct: 298 FPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPPSSLGGQPLGGP 357

Query: 245 DVLARPQRFAQLELSRAGLEQLEAGVGGRFRCS 278
+RP++ +LS + + G R CS
Sbjct: 358 G--SRPKK----KLSPPSISIDPPESQGSRRPPCS 385

FIG. 8

TEE007"8E30'650